SEQUENCE LISTING

<110> MASUDA, ESTEBAN

<120> METHODS OF SCREENING CYCLIC PEPTIDES AND IDENTIFYING TARGETS THEREFOR

<130> RIGL-023

<140> 10/533,144
<141> 2005-04-27

<150> US03/27370
<151> 2003-08-30

<150> 60/407,385
<151> 2002-08-30

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1227
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<220>
<221> CDS
<222> (1)...(1227)

<220>
<221> misc_feature
<222> 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171
<223> n = A,T,C or G

<400> 1

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atg gag agc ggc agc ccc gag atc gag aag ctg agt cag agc gac atc   48
Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1               5                  10                  15

tac tgg gac agc atg gtg agc atc acc gag acc ggc gtg gag gag gtg   96
Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
            20                  25                  30

ttc gac ctg acc gtg ccc ggc ccc cac aac ttc gtg gcc aac gac atc   144
Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
        35                  40                  45

atc gtc cac aac agc nnn nnn nnn nnn tgc atc agc ggc gac agc ctg   192
Ile Val His Asn Ser Xaa Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu
    50                  55                  60

atc agc ctg gcc agc acc ggc aag agg gtg agc atc aag gac ctg ctg   240
Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu
65                  70                  75                  80
```

```
gac gag aag gac ttc gag atc tgg gcc atc aac gag cag acc atg aag   288
Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys
                85                  90                  95

cta gag agc gcc aag gtg agc agg gtg ttc tgc acc ggc aag aag cta   336
Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu
            100                 105                 110

gtg tac atc cta aga acc agg cta ggc agg acc atc aag gcc acc gcc   384
Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala
        115                 120                 125

aac cac agg ttc cta acc atc gac ggc tgg aag agg cta gac gag cta   432
Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu
    130                 135                 140

agc cta aag gag cac atc gcc cta ccc cgg aag cta gag agc agc agc   480
Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser
145                 150                 155                 160

cta cag cta ggc ctc cgc ggc cag atc gat gtg agc aag ggc gag gag   528
Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu
                165                 170                 175

ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta   576
Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
            180                 185                 190

aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc   624
Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
        195                 200                 205

tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc   672
Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
    210                 215                 220

gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg cag tgc   720
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys
225                 230                 235                 240

ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc   768
Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
                245                 250                 255

gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac   816
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
            260                 265                 270

gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc   864
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
        275                 280                 285

ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc   912
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
    290                 295                 300

aac atc ctg ggg cac aag ctt gag tac aac ttc aac agc cac aac gtg   960
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
305                 310                 315                 320
```

```
tat atc atg gcc gac aag cag aag aac ggc atc aag gcc aac ttc aag   1008
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
                325                 330                 335

atc cgc cac aac atc gag gac gga tcc gtg cag ctc gcc gac cac tac   1056
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
            340                 345                 350

cag cag aac acc cca att ggc gac ggg ccc gtg ctg ctg ccc gac aac   1104
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
        355                 360                 365

cac tac ctg agc acc cag agc gct ctt tcg aaa gac ccc aac gag aag   1152
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
    370                 375                 380

cgc gat cat atg gtc ctg ctc gag ttc gtg acc gcc gcc ggg atc act   1200
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
385                 390                 395                 400

ctc ggc atg gac gag ctg tac aag taa                              1227
Leu Gly Met Asp Glu Leu Tyr Lys  *
                405
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<210> 2
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> 54, 55, 56, 57
<223> Xaa = Any Amino Acid

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<223> synthetic polypeptide

<400> 2

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Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1               5                  10                  15
Tyr Trp Asp Ser Met Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
            20                  25                  30
Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
        35                  40                  45
Ile Val His Asn Ser Xaa Xaa Xaa Xaa Cys Ile Ser Gly Asp Ser Leu
    50                  55                  60
Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu
65                  70                  75                  80
Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys
                85                  90                  95
Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu
            100                 105                 110
Val Tyr Ile Leu Arg Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala
        115                 120                 125
Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu
    130                 135                 140
Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser
145                 150                 155                 160
Leu Gln Leu Gly Leu Arg Gly Gln Ile Asp Val Ser Lys Gly Glu Glu
                165                 170                 175
```

```
Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
            180                 185                 190
Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
        195                 200                 205
Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
    210                 215                 220
Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val Gln Cys
225                 230                 235                 240
Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
                245                 250                 255
Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
            260                 265                 270
Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
        275                 280                 285
Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
    290                 295                 300
Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His Asn Val
305                 310                 315                 320
Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys
                325                 330                 335
Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
            340                 345                 350
Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
        355                 360                 365
His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
    370                 375                 380
Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
385                 390                 395                 400
Leu Gly Met Asp Glu Leu Tyr Lys
                405
```

<210> 3
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 3
Gly Ser Gly Gly Ser
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<210> 4
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 4
Ala Gly Pro Ile
1